



SEQUENCE LISTING

<110> Wong, Luet

<120> Process for oxidising terpenes

<130> P02196US0

<140> US 09/856,339

<141> 1999-11-19

<150> PCT/GB99/03873

<151> 1998-11-19

<160> 24

<170> PatentIn version 3.1

<210> 1

<211> 1242

<212> DNA

<213> Pseudomonas putida

<220>

<221> misc_feature

<222> (1)..(1242)

<223> Coding Sequence

<400> 1

acgactgaaa ccatacaaag caacgccaat cttgcccctc tgccacccca tgtgccagag	60
cacctgggtat tcgacttcga catgtacaat ccgtcgaatc tgtctgccgg cgtgcaggag	120
gcctggggcag ttctgcaaga atcaaacgta ccggatctgg tgtggactcg ctgcaacggc	180
ggacactgga tcgccactcg cggccaactg atccgtgagg cctatgaaga ttaccgccac	240
ttttccagcg agtgcccgtt catccctcgt gaagccggcg aagcctacga cttcattccc	300
acctcgatgg atccgcccga gcagcgccag ttctgtgcgc tggccaacca agtggttggc	360
atgccggtgg tggataagct ggagaaccgg atccaggagc tggcctgctc gctgatcgag	420
agcctgcgcc cgcaaggaca gtgcaacttc accgaggact acgccgaacc cttcccata	480
cgcattctca tgctgctcgc aggtctaccg gaagaagata tcccgcactt gaaataccta	540
acggatcaga tgaccctgcc ggatggcagc atgaccttcg cagaggccaa ggaggcgctc	600
tacgactatc tgataccgat catcgagcaa cgcaggcaga agccgggaac cgacgctatc	660
agcatcggtg ccaacggcca ggtcaatggg cgaccgatca ccagtgcga agccaagagg	720
atgtgtggcc tgttactggt cggcggcctg gatacgggtg tcaatttctc cagcttcagc	780
atggagttcc tggccaaaag cccggagcat cgccaggagc tgatcgagcg tcccagagct	840
attccagccg cttgcgagga actactccgg cgcttctcgc tggttgccga tggccgcac	900
ctcacctccg attacgagtt tcatggcggtg caactgaaga aaggtgacca gatcctgcta	960

ccgcagatgc tgtctggcct ggatgagcgc gaaaacgcct gcccgatgca cgtcgacttc	1020
agtcgccaaa aggtttcaca caccaccttt ggccacggca gccatctgtg ctttggccag	1080
cacctggccc gccgggaaat catcgtcacc ctcaaggaat ggctgaccag gattcctgac	1140
ttctccattg ccccggtgc ccagattcag cacaagagcg gcacgtcag cggcgtgcag	1200
gcactccctc tggctctggga tccggcgact accaaagcgg ta	1242

<210> 2
 <211> 3150
 <212> DNA
 <213> Bacillus megaterium

<220>
 <221> misc_feature
 <222> (1)..(3150)
 <223> Coding Sequence

<400> 2	
atgacaatta aagaaatgcc tcagccaaaa acgtttggag agcttaaaaa ttaccgtta	60
ttaaacacag ataaaccggt tcaagctttg atgaaaattg cggatgaatt aggagaaatc	120
tttaaattcg aggcgcctgg tcgtgtaacg cgctacttat caagtcagcg tctaattaaa	180
gaagcatgcg atgaatcacg ctttgataaa aacttaagtc aagcgcttaa atttgtacgt	240
gattttgcag gagacggggt atttacaagc tggacgcag aaaaaaattg gaaaaaagcg	300
cataatatct tacttccaag cttcagtcag caggcaatga aaggctatca tgcgatgatg	360
gtcgatatcg ccgtgcagct tgttcaaaag tgggagcgtc taaatgcaga tgagcatatt	420
gaagtaccgg aagacatgac acgtttaacg cttgatacaa ttggtctttg cggctttaac	480
tatcgcttta acagctttta ccgagatcag cctcatccat ttattacaag tatggtcctg	540
gcactggatg aagcaatgaa caagctgcag cgagcaaadc cagacgaccc agcttatgat	600
gaaaacaagc gccagtttca agaagatatc aaggatgatga acgacctagt agataaaatt	660
attgcagatc gcaaagcaag cggatgaaca agcgatgatt tattaacgca tatgctaaac	720
ggaaaagatc cagaaacggg tgagccgctt gatgacgaga acattcgcta tcaaattatt	780
acattcttaa ttgcgggaca cgaaacaaca agtgggtcttt tatcatttgc gctgtatttc	840
ttagtgaaaa atccacatgt attacaaaaa gcagcagaag aagcagcacg agttctagta	900
gatcctgctc caagctacaa acaagtcaaa cagcttaaat atgtcggcat ggtcttaaac	960
gaagcgctgc gcttatggcc aactgctcct gcgttttccc tatatgcaaa agaagatacg	1020
gtgcttggag gagaatatcc tttagaaaaa ggcgacgaac taatgggttct gattcctcag	1080
cttcaccgtg ataaaacaat ttggggagac gatgtggaag agttccgtcc agagcgtttt	1140

gaaaatccaa	gtgcgattcc	gcagcatgcg	tttaaaccgt	ttggaaacgg	tcagcgtgcg	1200
tgtatcgggtc	agcagttcgc	tcttcatgaa	gcaacgctgg	tacttggtat	gatgctaaaa	1260
cactttgact	ttgaagatca	tacaaactac	gagctggata	ttaaagaaac	tttaacgtta	1320
aaacctgaag	gctttgtggt	aaaagcaaaa	tcgaaaaaaa	ttccgcttgg	cggtattcct	1380
tcacctagca	ctgaacagtc	tgccaaaaaa	gcacgcaaaa	aggcagaaaa	cgctcataat	1440
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cgcctgata	acgcaaagca	atttgtcgac	tggttagacc	aagcgtctgc	tgatgaagta	1680
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cgcggtgaag	cagatgcaag	cgacgacttt	gaaggcacat	atgaagaatg	gcgtgaacat	1860
atgtggagtg	acgtagcagc	ctactttaac	ctcgacattg	aaaacagtga	agataataaa	1920
tctactcttt	cacttcaatt	tgtcgacagc	gccgcggata	tgccgcttgc	gaaaatgcac	1980
ggtgcgtttt	caacgaacgt	cgtagcaagc	aaagaacttc	aacagccagg	cagtgcacga	2040
agcacgcgac	atcttgaaat	tgaacttcca	aaagaagctt	cttatcaaga	aggagatcat	2100
ttaggtgtta	ttcctcgcaa	ctatgaagga	atagtaaacc	gtgtaacagc	aagggttcggc	2160
ctagatgcat	cacagcaaat	ccgtctggaa	gcagaagaag	aaaaattāgc	tcatttgcca	2220
ctcgctaaaa	cagtatccgt	agaagagctt	ctgcaatacg	tggagcttca	agatcctggt	2280
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cttgaagcct	tgcttgaaaa	gcaagcctac	aaagaacaag	tgctggcaaa	acgtttaaca	2400
atgcttgaac	tgcttgaaaa	ataccggcg	tgtgaaatga	aattcagcga	atttatcgcc	2460
cttctgccaa	gcatacgccc	gcgctattac	tcgatttctt	catcacctcg	tgtcgatgaa	2520
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tataaaggaa	ttgcgtcgaa	ctatcttgcc	gagctgcaag	aaggagatac	gattacgtgc	2640
tttatttcca	caccgcagtc	agaattttacg	ctgccaaaag	accctgaaac	gccgcttatc	2700
atggctcggac	cgggaacagg	cgtcgcgcgcg	tttagaggct	ttgtgcaggc	gcgcaaacag	2760
ctaaaagaac	aaggacagtc	acttgagaa	gcacatttat	acttcggctg	ccgttcacct	2820
catgaagact	atctgtatca	agaagagctt	gaaaacgccc	aaagcgaagg	catcattacg	2880
cttcataccg	ctttttctcg	catgccaaat	cagccgaaaa	catacgttca	gcacgtaatg	2940

gaacaagacg gcaagaaatt gattgaactt cttgatcaag gagcgcaactt ctatatttgc 3000
ggagacggaa gccaaatggc acctgccgtt gaagcaacgc ttatgaaaag ctatgctgac 3060
gttcaccaag tgagtgaagc agacgctcgc ttatggctgc agcagctaga agaaaaaggc 3120
cgatacgcaa aagacgtgtg ggctgggtaa 3150

<210> 3
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<220>
<221> DOMAIN
<222> (1)..(7)
<223> Linker

<400> 3

Thr Asp Gly Thr Ser Ser Thr
1 5

<210> 4
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<220>
<221> DOMAIN
<222> (1)..(7)
<223> Linker

<400> 4

Thr Asp Gly Ala Ser Ser Ser
1 5

<210> 5
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<220>
<221> DOMAIN
<222> (1)..(17)
<223> Linker

<400> 5

Thr Asp Gly Thr Arg Pro Gly Pro Gly Pro Gly Pro Gly Pro Ser Ser
1 5 10 15

Thr

<210> 6
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<220>
<221> DOMAIN
<222> (1)..(21)
<223> Linker

<400> 6

Thr Asp Gly Thr Arg Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro
1 5 10 15

Gly Pro Ser Ser Thr
20

<210> 7
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<220>
<221> DOMAIN
<222> (1)..(4)
<223> Linker

<400> 7

Pro Leu Glu Leu
1

<210> 8
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<220>
<221> DOMAIN
<222> (1)..(7)
<223> Linker

<400> 8

Thr Asp Gly Gly Ser Ser Ser
1 5

<210> 9
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (1)..(51)
<223> Primer

<400> 9
gagattaaga attcataaac acatgggagt gcgtgccata tgaacgcaaa c

51

<210> 10
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding Sequence

<220>
<221> variation
<222> (1)..(36)
<223> Desired coding sequence

<400> 10
gaactgagta gtgccactga cggaggatcc tcatcg

36

<210> 11
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature

<222> (1)..(36)
<223> Primer

<400> 11
cgatgaggat cctccgtcag tggcactact cagttc

36

<210> 12
<211> 36
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> Primer

<220>
<221> misc_feature
<222> (1)..(36)
<223> Primer

<400> 12
tcatcgggat cctcatcgat gtctaaagta gtgtat

36

<210> 13
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Desired Coding Sequence

<220>
<221> misc_feature
<222> (1)..(52)
<223> Desired Coding Sequence

<400> 13
cccgataggc aatggtaatc atcgggagtc tagagcatcg aagctttcat cg

52

<210> 14
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (1)..(52)
<223> Primer

<400> 14
cgatgaaagc ttcgatgctc tagactcccg atgattacca ttgcctatcg gg

52

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (1)..(24)
<223> Primer

<400> 15
tcatcgacgc gtcgcgaact gctg

24

<210> 16
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Desired Coding Sequence

<220>
<221> misc_feature
<222> (1)..(69)
<223> Desired Coding Sequence

<400> 16
cccgataggc aatggtaagt aggtgaatat ctaatcccca tctatgcgcg agtggagtct
agagttcga

60

69

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (1)..(21)
<223> Primer

<400> 17
tcatcgaagc ttggctgttt t

21

<210> 18
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Desired Coding Sequence

<220>
<221> misc_feature
<222> (1)..(47)
<223> Desired Coding Sequence

<400> 18
acaatttcac acaggatcta gaccatatgt catcgaagct ttcacg

47

<210> 19
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (1)..(47)
<223> Primer

<400> 19
cgatgaaagc ttcgatgaca tatggtctag atcctgtgtg aaattgt

47

<210> 20
<211> 414
<212> PRT
<213> Pseudomonas putida

<220>
<221> MUTAGEN
<222> (1)..(414)
<223> Coding sequence

<400> 20

Thr Thr Glu Thr Ile Gln Ser Asn Ala Asn Leu Ala Pro Leu Pro Pro
1 5 10 15

His Val Pro Glu His Leu Val Phe Asp Phe Asp Met Tyr Asn Pro Ser
20 25 30

Asn Leu Ser Ala Gly Val Gln Glu Ala Trp Ala Val Leu Gln Glu Ser
35 40 45

Asn Val Pro Asp Leu Val Trp Thr Arg Cys Asn Gly Gly His Trp Ile
50 55 60

Ala Thr Arg Gly Gln Leu Ile Arg Glu Ala Tyr Glu Asp Tyr Arg His
 65 70 75 80

Phe Ser Ser Glu Cys Pro Phe Ile Pro Arg Glu Ala Gly Glu Ala Tyr
 85 90 95

Asp Phe Ile Pro Thr Ser Met Asp Pro Pro Glu Gln Arg Gln Phe Arg
 100 105 110

Ala Leu Ala Asn Gln Val Val Gly Met Pro Val Val Asp Lys Leu Glu
 115 120 125

Asn Arg Ile Gln Glu Leu Ala Cys Ser Leu Ile Glu Ser Leu Arg Pro
 130 135 140

Gln Gly Gln Cys Asn Phe Thr Glu Asp Tyr Ala Glu Pro Phe Pro Ile
 145 150 155 160

Arg Ile Phe Met Leu Leu Ala Gly Leu Pro Glu Glu Asp Ile Pro His
 165 170 175

Leu Lys Tyr Leu Thr Asp Gln Met Thr Arg Pro Asp Gly Ser Met Thr
 180 185 190

Phe Ala Glu Ala Lys Glu Ala Leu Tyr Asp Tyr Leu Ile Pro Ile Ile
 195 200 205

Glu Gln Arg Arg Gln Lys Pro Gly Thr Asp Ala Ile Ser Ile Val Ala
 210 215 220

Asn Gly Gln Val Asn Gly Arg Pro Ile Thr Ser Asp Glu Ala Lys Arg
 225 230 235 240

Met Cys Gly Leu Leu Leu Val Gly Gly Leu Asp Thr Val Val Asn Phe
 245 250 255

Leu Ser Phe Ser Met Glu Phe Leu Ala Lys Ser Pro Glu His Arg Gln
 260 265 270

Glu Leu Ile Glu Arg Pro Glu Arg Ile Pro Ala Ala Cys Glu Glu Leu
 275 280 285

Leu Arg Arg Phe Ser Leu Val Ala Asp Gly Arg Ile Leu Thr Ser Asp
 290 295 300

Tyr Glu Phe His Gly Val Gln Leu Lys Lys Gly Asp Gln Ile Leu Leu

305 310 315 320
 Pro Gln Met Leu Ser Gly Leu Asp Glu Arg Glu Asn Ala Cys Pro Met
 325 330 335
 His Val Asp Phe Ser Arg Gln Lys Val Ser His Thr Thr Phe Gly His
 340 345 350
 Gly Ser His Leu Cys Leu Gly Gln His Leu Ala Arg Arg Glu Ile Ile
 355 360 365
 Val Thr Leu Lys Glu Trp Leu Thr Arg Ile Pro Asp Phe Ser Ile Ala
 370 375 380
 Pro Gly Ala Gln Ile Gln His Lys Ser Gly Ile Val Ser Gly Val Gln
 385 390 395 400
 Ala Leu Pro Leu Val Trp Asp Pro Ala Thr Thr Lys Ala Val
 405 410

 <210> 21
 <211> 1049
 <212> PRT
 <213> bacillus megaterium

 <220>
 <221> MUTAGEN
 <222> (1)..(1049)
 <223> Coding Sequence

 <400> 21
 Met Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys
 1 5 10 15
 Asn Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys
 20 25 30
 Ile Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg
 35 40 45
 Val Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp
 50 55 60
 Glu Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg
 65 70 75 80
 Asp Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn

85

90

95

Trp Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala
 100 105 110

Met Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val
 115 120 125

Gln Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu
 130 135 140

Asp Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn
 145 150 155 160

Tyr Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr
 165 170 175

Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala
 180 185 190

Asn Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu
 195 200 205

Asp Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg
 210 215 220

Lys Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn
 225 230 235 240

Gly Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg
 245 250 255

Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly
 260 265 270

Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu
 275 280 285

Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Ala Pro
 290 295 300

Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn
 305 310 315 320

Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala
 325 330 335

Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp
340 345 350

Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp
355 360 365

Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser
370 375 380

Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala
385 390 395 400

Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly
405 410 415

Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu
420 425 430

Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys
435 440 445

Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr
450 455 460

Glu Gln Ser Ala Lys Lys Ala Arg Lys Lys Ala Glu Asn Ala His Asn
465 470 475 480

Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly
485 490 495

Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro
500 505 510

Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly
515 520 525

Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn
530 535 540

Ala Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val
545 550 555 560

Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala
565 570 575

Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala
580 585 590

Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp
595 600 605

Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp
610 615 620

Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys
625 630 635 640

Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu
645 650 655

Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu
660 665 670

Leu Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu
675 680 685

Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile
690 695 700

Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly
705 710 715 720

Leu Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu
725 730 735

Ala His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln
740 745 750

Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met
755 760 765

Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu
770 775 780

Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr
785 790 795 800

Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser
805 810 815

Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile
820 825 830

Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser
835 840 845

Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile
850 855 860

Ala Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys
865 870 875 880

Phe Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu
885 890 895

Thr Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg
900 905 910

Gly Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu
915 920 925

Gly Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr
930 935 940

Leu Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr
945 950 955 960

Leu His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val
965 970 975

Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp
980 985 990

Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro
995 1000 1005

Ala Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln
1010 1015 1020

Val Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu
1025 1030 1035

Lys Gly Arg Tyr Ala Lys Asp Val Trp Ala Gly
1040 1045

<210> 22

<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Coding Sequence

<220>
<221> MUTAGEN
<222> (1)..(5)
<223> Coding Sequence

<400> 22

Thr Asp Gly Gly Ser
1 5

<210> 23
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> MUTAGEN
<222> (1)..(2)
<223> Primer

<400> 23

Gly Ser
1

<210> 24
<211> 1048
<212> PRT
<213> Bacillus megaterium

<220>
<221> MUTAGEN
<222> (1)..(1048)
<223> Coding Sequence

<400> 24

Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys Asn
1 5 10 15

Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys Ile
20 25 30

Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val

35					40					45					
Thr	Arg	Tyr	Leu	Ser	Ser	Gln	Arg	Leu	Ile	Lys	Glu	Ala	Cys	Asp	Glu
50					55					60					
Ser	Arg	Phe	Asp	Lys	Asn	Leu	Ser	Gln	Ala	Leu	Lys	Phe	Val	Arg	Asp
65					70					75					80
Phe	Ala	Gly	Asp	Gly	Leu	Phe	Thr	Ser	Trp	Thr	His	Glu	Lys	Asn	Trp
				85					90					95	
Lys	Lys	Ala	His	Asn	Ile	Leu	Leu	Pro	Ser	Phe	Ser	Gln	Gln	Ala	Met
			100					105					110		
Lys	Gly	Tyr	His	Ala	Met	Met	Val	Asp	Ile	Ala	Val	Gln	Leu	Val	Gln
		115					120					125			
Lys	Trp	Glu	Arg	Leu	Asn	Ala	Asp	Glu	His	Ile	Glu	Val	Pro	Glu	Asp
	130					135					140				
Met	Thr	Arg	Leu	Thr	Leu	Asp	Thr	Ile	Gly	Leu	Cys	Gly	Phe	Asn	Tyr
145					150					155					160
Arg	Phe	Asn	Ser	Phe	Tyr	Arg	Asp	Gln	Pro	His	Pro	Phe	Ile	Thr	Ser
				165					170					175	
Met	Val	Arg	Ala	Leu	Asp	Glu	Ala	Met	Asn	Lys	Leu	Gln	Arg	Ala	Asn
			180					185					190		
Pro	Asp	Asp	Pro	Ala	Tyr	Asp	Glu	Asn	Lys	Arg	Gln	Phe	Gln	Glu	Asp
		195					200					205			
Ile	Lys	Val	Met	Asn	Asp	Leu	Val	Asp	Lys	Ile	Ile	Ala	Asp	Arg	Lys
	210					215					220				
Ala	Ser	Gly	Glu	Gln	Ser	Asp	Asp	Leu	Leu	Thr	His	Met	Leu	Asn	Gly
225					230					235					240
Lys	Asp	Pro	Glu	Thr	Gly	Glu	Pro	Leu	Asp	Asp	Glu	Asn	Ile	Arg	Tyr
				245					250					255	
Gln	Ile	Ile	Thr	Phe	Leu	Ile	Ala	Gly	His	Glu	Thr	Thr	Ser	Gly	Leu
			260					265					270		
Leu	Ser	Phe	Ala	Leu	Tyr	Phe	Leu	Val	Lys	Asn	Pro	His	Val	Leu	Gln
			275				280					285			

Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Ala Pro Ser
 290 295 300

Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu
 305 310 315 320

Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala Lys
 325 330 335

Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp Glu
 340 345 350

Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly
 355 360 365

Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala
 370 375 380

Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala Cys
 385 390 395 400

Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly Met
 405 410 415

Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu Asp
 420 425 430

Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys Ala
 435 440 445

Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr Glu
 450 455 460

Gln Ser Ala Lys Lys Ala Arg Lys Lys Ala Glu Asn Ala His Asn Thr
 465 470 475 480

Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly Thr
 485 490 495

Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro Gln
 500 505 510

Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly Ala
 515 520 525

Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn Ala
 530 535 540

Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val Lys
 545 550 555 560

Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala Thr
 565 570 575

Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala Lys
 580 585 590

Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp Asp
 595 600 605

Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp Val
 610 615 620

Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys Ser
 625 630 635 640

Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu Ala
 645 650 655

Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu Leu
 660 665 670

Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu Leu
 675 680 685

Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile Pro
 690 695 700

Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly Leu
 705 710 715 720

Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu Ala
 725 730 735

His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln Tyr
 740 745 750

Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met Ala
 755 760 765

Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu Leu
 770 775 780

Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr Met
 785 790 795 800

Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser Glu
 805 810 815

Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile Ser
 820 825 830

Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser Val
 835 840 845

Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile Ala
 850 855 860

Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys Phe
 865 870 875 880

Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu Thr
 885 890 895

Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly
 900 905 910

Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu Gly
 915 920 925

Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr Leu
 930 935 940

Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr Leu
 945 950 955 960

His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln
 965 970 975

His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln
 980 985 990

Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala
 995 1000 1005

Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val

1010

1015

1020

Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys
1025 1030 1035

Gly Arg Tyr Ala Lys Asp Val Trp Ala Gly
1040 1045